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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=5; day=8; hr=14; min=47; sec=42; ms=77;]

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Reviewer Comments:

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur F?rung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

Missing headings because of the non-ascii character which is shown in the above attachment.

Application No: 10586111 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-24 16:19:26.908
Finished: 2008-04-24 16:19:28.281
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 373 ms
Total Warnings: 9
Total Errors: 3
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)

<210> 1
<211> 1785
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>
<221> CDS
<222> (1)..(1785)

<220>
<221> N_region
<222> (1)..(21)
<223> immunoglobulin kappa chain leader sequence

<400> 1
atg gag aca gac aca ctc ctg cta tgg gta ctg ctg tgg gtt cca 48
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

ggt tcc act ggt gac tct aga atg gtc cag gcc tcg atg agg agc cca 96
Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro
20 25 30

aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att 144
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
35 40 45

gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg 192
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
50 55 60

gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg 240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
65 70 75 80

cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg 288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
85 90 95

gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg 336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
100 105 110

cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta 384
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
115 120 125

gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tcg tta 432
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
130 135 140

agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg 480
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val

145	150	155	160	
aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa				528
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu				
165	170	175		
aac atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg				576
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu				
180	185	190		
att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa				624
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys				
195	200	205		
aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat				672
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr				
210	215	220		
gag cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc				720
Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr				
225	230	235	240	
tat atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa				768
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln				
245	250	255		
gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa				816
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu				
260	265	270		
ttc ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt				864
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu				
275	280	285		
ctt gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga				912
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg				
290	295	300		
cat ccc tgg atc gga tcc aaa cta gct gag cac gaa ggt gac gcg gcc				960
His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala				
305	310	315	320	
cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act gaa ctg				1008
Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu				
325	330	335		
gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct ggc tac				1056
Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr				
340	345	350		
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag				1104
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln				
355	360	365		
ggt ctg gaa tgg att gga tac att aat cct aac act gct tat act gac				1152
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp				
370	375	380		

tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac aaa tcc			1200
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser			
385	390	395	400
tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag gat tct			1248
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser			
405	410	415	
gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt			1296
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe			
420	425	430	
cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc			1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly			
435	440	445	
ggt tca ggc gga ggt ggc tct ggc ggt gga tcg gac att gtg ctg			1392
Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Val Leu			
450	455	460	
acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg gtc acc			1440
Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr			
465	470	475	480
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat			1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr			
485	490	495	
caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc			1536
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser			
500	505	510	
aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga tct gga			1584
Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly			
515	520	525	
aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac ctt gca			1632
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala			
530	535	540	
gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc ggt gct			1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala			
545	550	555	560
ggc acc aag ctg gaa atc aaa cgg gcg gcc gca ggg ccc gaa caa aaa			1728
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Pro Glu Gln Lys			
565	570	575	
ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat			1776
Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His			
580	585	590	
cat cat tga			1785
His His			
595			

<210> 2
<211> 594
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:
pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro
20 25 30
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
35 40 45
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
50 55 60
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
65 70 75 80
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
85 90 95
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
100 105 110
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
115 120 125
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
130 135 140
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val
145 150 155 160
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu
165 170 175
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu
180 185 190
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys
195 200 205
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
210 215 220
Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr
225 230 235 240
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
245 250 255
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
260 265 270
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
275 280 285
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
290 295 300
His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala
305 310 315 320
Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu
325 330 335
Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
340 345 350
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln
355 360 365
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp
370 375 380

Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser
 385 390 395 400
 Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser
 405 410 415
 Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe
 420 425 430
 Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 435 440 445
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Val Leu
 450 455 460
 Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr
 465 470 475 480
 Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr
 485 490 495
 Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser
 500 505 510
 Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly
 515 520 525
 Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
 530 535 540
 Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala
 545 550 555 560
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Pro Glu Gln Lys
 565 570 575
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 580 585 590
 His His

<210> 3
 <211> 1794
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

<220>
 <221> CDS
 <222> (1)..(1794)

<220>
 <221> N_region
 <222> (1)..(21)
 <223> immunoglobulin kappa chain leader sequence

<400> 3
 atg gag aca gac aca ctc ctg cta tgg gta ctg ctg tgg gtt cca 48
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 ggt tcc act ggt gac gca gcc cag ccc gcc atg gcc cag gtc aag ctg 96
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
 20 25 30

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met 35 40 45	144
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp 50 55 60	192
gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn 65 70 75 80	240
cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala 85 90 95	288
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Arg 100 105 110	336
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr 115 120 125	384
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val 130 135 140	432
acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt Thr Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly 145 150 155 160	480
ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met 165 170 175	528
tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val 180 185 190	576
gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 195 200 205	624
ctg ctg ata tac ggg gcc tcc aac cgg tac act ggg gtc ccc gat cgc Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg 210 215 220	672
ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser 225 230 235 240	720
gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag aat tac agg Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg 245 250 255	768
tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg	816

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
260 265 270

gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat 864
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
275 280 285

atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga 912
Met Glu Thr Phe Lys Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
290 29